

**BLASTP 2.2.8 [Jan-05-2004]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

RID: 1079122645-18035-203521758519.BLASTQ3

Query=

(264 letters)

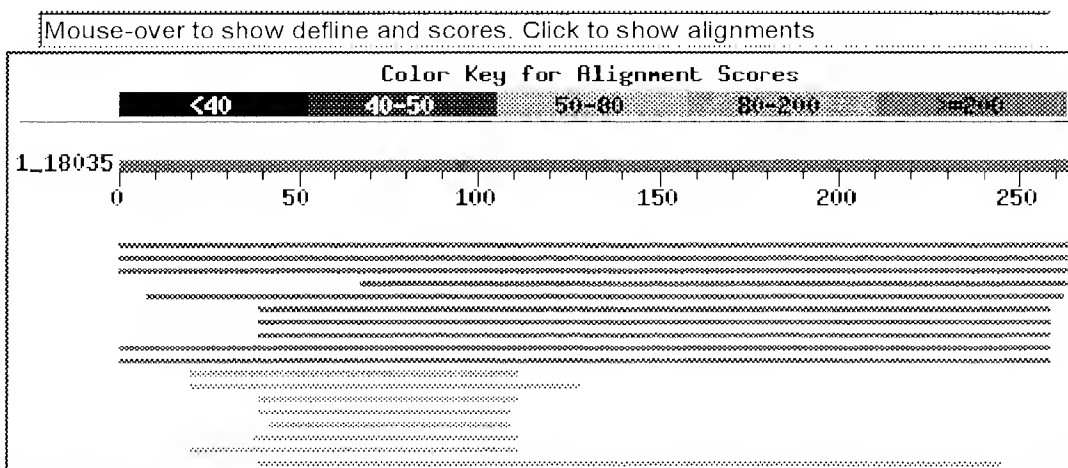
Database: All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF

2,678,069 sequences; 748,330,716 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 1058 Blast Hits on the Query Sequence



Sequences producing significant alignments:

Score E
(bits) Value

gi 13128972 ref NP_076932.1 	collectin sub-family member 11...	812	0.0	
gi 38049424 ref XP_283054.2 	collectin sub-family member 11...	726	0.0	
gi 34863397 ref XP_345653.1 	similar to hypothetical protei...	719	0.0	

gi 40548420 ref NP_954705.1	collectin sub-family member 11...	608	e-173	
gi 33417124 gb AAH56052.1	Colec11-prov protein [Xenopus la...	569	e-161	
gi 27718901 ref XP_235330.1	similar to collectin liver 1; ...	246	9e-64	
gi 5453619 ref NP_006429.1	collectin sub-family member 10;...	244	4e-63	
gi 37183194 gb AAQ89397.1	COLEC10 [Homo sapiens]	239	1e-61	
gi 27734138 ref NP_775598.1	collectin liver 1; collectin-L...	234	3e-60	
gi 27530341 dbj BAC53954.1	collectin-L1 [Mus musculus]	233	6e-60	
gi 7656989 ref NP_056534.1	collagen, type V, alpha 3 prepr...	79	3e-13	
gi 9453886 dbj BAB03287.1	pro-alpha 1 type V/XI collagen [...]	77	1e-12	
gi 13994280 ref NP_114117.1	Clq and tumor necrosis factor ...	77	1e-12	
gi 13560506 gb AAK30079.1	collagen-like protein B [Strepto...	74	6e-12	
gi 11096157 gb AAG30218.1	collagen-like surface protein [S...	74	6e-12	
gi 11096147 gb AAG30213.1	collagen-like surface protein [S...	74	1e-11	
gi 841122 gb AAA67751.1	putative collagen alpha-2 (XI) cha...	73	1e-11	
gi 6753482 ref NP_034056.1	procollagen, type XI, alpha 2 [...]	73	1e-11	
gi 11096159 gb AAG30219.1	collagen-like surface protein [S...	73	1e-11	
gi 30316381 sp Q64739 CA2B_MOUSE	Collagen alpha 2(XI) chain...	73	1e-11	
gi 34852201 ref XP_215342.2	similar to Collagen alpha 2(XI...	73	1e-11	
gi 43221771 gb EAC76447.1	unknown [environmental sequence]	73	2e-11	
gi 31239123 ref XP_319975.1	ENSANGP00000016783 [Anopheles ...]	72	3e-11	
gi 9632525 ref NP_049519.1	putative tail fiber protein [Ba...	71	5e-11	
gi 29549 emb CAA68698.1	unnamed protein product [Homo sapi...	71	5e-11	
gi 6759903 gb AAI28099.1	alpha 1 (V) collagen [Gallus gallus]	71	5e-11	
gi 28703797 gb AAH47305.1	COL4A1 protein [Homo sapiens]	71	5e-11	
gi 12314281 emb CAC13153.1	ba472K17.2 (collagen type IV al...	71	5e-11	
gi 7656985 ref NP_001836.1	alpha 1 type IV collagen prepro...	71	5e-11	
gi 7649887 dbj BAA94165.1	tail fiber protein [Escherichia ...]	71	5e-11	
gi 19848250 gb UWL99382.1	collagen IV alpha 1 chain [Anoph...	71	5e-11	
gi 225874 prf 1402236A	collagen alpha1(IV)	71	5e-11	
gi 1173848 gb AAB41374.1	type V collagen	71	5e-11	
gi 115313 sp P20908 CA15_HUMAN	Collagen alpha 1(V) chain pr...	71	6e-11	
gi 1260669 pir ICGHU1V	collagen alpha 1(V) chain precursor ...	71	6e-11	
gi 16554579 ref NP_000084.2	alpha 1 type V collagen prepro...	71	6e-11	
gi 38014150 gb AAH08760.3	COL5A1 protein [Homo sapiens]	71	6e-11	
gi 6680958 ref NP_031755.1	procollagen, type XI, alpha 1; ...	71	8e-11	
gi 2119157 pir JX0363	collagen alpha 1(XIX) chain precurs...	70	1e-10	
gi 23468285 gb AAH38308.1	Clqtnf7 protein [Mus musculus]	70	1e-10	
gi 8393173 ref NP_058615.1	procollagen, type V, alpha 3; P...	70	1e-10	
gi 34878304 ref XP_223507.2	similar to Clqtnf7 protein [Ra...	70	1e-10	
gi 10281667 ref NP_001848.1	alpha 1 type XIX collagen prec...	70	1e-10	
gi 30425140 ref NP_780634.1	Clq and tumor necrosis factor ...	70	1e-10	
gi 292352 gb AAA36358.1	collagen	70	1e-10	
gi 182387 gb AAA58468.1	fibril-associated collagen	70	1e-10	
gi 624871 dbj BAA07368.1	al(XIX) collagen chain precursor ...	70	1e-10	
gi 44637832 gb EAK65704.1	unknown [environmental sequence]	70	2e-10	
gi 476846 pir A45748	collagen alpha 1(VII) chain - mouse (...)	70	2e-10	
gi 7656987 ref NP_056549.1	procollagen, type V, alpha 1; p...	70	2e-10	
gi 283868 pir S28791	collagen alpha 1(XI) chain - chicken ...	70	2e-10	
gi 6680972 ref NP_031764.1	procollagen, type VII, alpha 1 ...	70	2e-10	

gi 34859869 ref XP_342327.1 	procollagen type XI alpha 1 [R...	69	2e-10	
gi 30354436 gb AAH52161.1 	Procollagen, type XI, alpha 1 [M...	69	2e-10	
gi 11120719 ref NP_068528.1 	collagen, type V, alpha 3; pro...	69	2e-10	
gi 115347 sp P27393 CA24_ASCSU	Collagen alpha 2(IV) chain p...	69	2e-10	
gi 3172000 emb CAA06511.1 	collagen alpha 1 (XI) [Rattus no...	69	2e-10	
gi 11096145 gb AAG30212.1 	collagen-like surface protein [S...	69	2e-10	
gi 115328 sp P20909 CA1B_RAT	COLLAGEN ALPHA 1(XI) CHAIN >gi...	69	2e-10	
gi 29566025 ref NP_817595.1 	gp4 [Mycobacteriophage Bxz2] >...	69	3e-10	
gi 30145636 emb CAD89749.1 	C. elegans COL-135 protein (cor...	69	3e-10	
gi 11096151 gb AAG30215.1 	collagen-like surface protein [S...	69	4e-10	
gi 423287 pir S33603	surfactant protein D - bovine	69	4e-10	
gi 4502961 ref NP_000085.1 	alpha 1 type VII collagen precu...	69	4e-10	
gi 44173973 gb EAAH52456.1 	unknown [environmental sequence]	69	4e-10	
gi 2137076 pir I48103	type VII collagen - Chinese hamster ...	69	4e-10	
gi 31217994 ref XP_316546.1 	WNSANGP00000010005 [Anopheles ...	69	5e-10	
gi 37722541 gb AAO06817.1 	asymmetric acetylcholinesterase ...	68	7e-10	
gi 37722545 gb AAO06819.1 	asymmetric acetylcholinesterase ...	68	7e-10	
gi 7239359 gb AAF43197.1 	acetylcholinesterase collagen-lik...	68	7e-10	
gi 18105030 ref NP_536805.1 	acetylcholinesterase collagen-...	68	7e-10	
gi 180715 gb AAA52034.1 	alpha-2 type XI collagen	68	7e-10	
gi 18201917 ref NP_542411.1 	alpha 2 type XI collagen isofo...	68	7e-10	
gi 1360671 pir CGHU2E	collagen alpha 2(XI) chain precursor...	68	7e-10	
gi 1000747 gb AAC50215.1 	Pro-a2(XI)	68	7e-10	
gi 18201919 ref NP_542412.1 	alpha 2 type XI collagen isofo...	68	7e-10	
gi 37722539 gb AAO06816.1 	asymmetric acetylcholinesterase ...	68	7e-10	
gi 18105022 ref NP_536801.1 	acetylcholinesterase collagen-...	68	7e-10	
gi 18105028 ref NP_536804.1 	acetylcholinesterase collagen-...	68	7e-10	
gi 12643842 sp Q9Y215 COLO_HUMAN	Acetylcholinesterase colla...	68	7e-10	
gi 13432104 sp P13942 CA2B_HUMAN	Collagen alpha 2(XI) chain...	68	7e-10	
gi 3820987 emb CAA20240.1 	dJ1033B10.12 (collagen, type XI,...	68	7e-10	
gi 18201915 ref NP_542410.1 	alpha 2 type XI collagen isofo...	68	7e-10	
gi 1000746 gb AAC50214.1 	Pro-a2(XI) >gi 1584719 prf 21233...	68	7e-10	
gi 37722543 gb AAO06818.1 	asymmetric acetylcholinesterase ...	68	7e-10	
gi 18105024 ref NP_536802.1 	acetylcholinesterase collagen-...	68	7e-10	
gi 1000745 gb AAC50213.1 	Pro-a2(XI)	68	7e-10	
gi 18105016 ref NP_005668.2 	acetylcholinesterase collagen-...	68	7e-10	
gi 18105018 ref NP_536799.1 	acetylcholinesterase collagen-...	68	7e-10	
gi 18105020 ref NP_536800.1 	acetylcholinesterase collagen-...	68	7e-10	
gi 11875612 gb AAG40729.1 	type IV collagen alpha 1 chain p...	67	9e-10	
gi 18780273 ref NP_110447.2 	alpha 1 type XXI collagen prec...	67	9e-10	
gi 19745166 ref NP_604447.1 	collagen, type V, alpha 1 [Rat...	67	9e-10	
gi 6165881 gb AAF04724.1 	collagen type XI alpha-1 [Homo sa...	67	9e-10	
gi 18375522 ref NP_542197.1 	alpha 1 type XI collagen isofo...	67	9e-10	
gi 6165882 gb AAF04725.1 	collagen type XI alpha-1 isoform ...	67	9e-10	
gi 7441219 pir S18803	collagen alpha 1(V) chain - hamster	67	9e-10	
gi 18375518 ref NP_001845.2 	alpha 1 type XI collagen isofo...	67	9e-10	
gi 1360670 pir CGHU1E	collagen alpha 1(XI) chain precursor...	67	9e-10	
gi 33149359 gb AAO64414.1 	type VII collagen [Canis familia...	67	9e-10	

Alignments

Get selected sequences

Select all

Deselect all

>gi|13123972|ref|NP_076932.1| collectin sub-family member 11 isoform a [Homo s
 gi|12652661|gb|AAH00078.1| Collectin sub-family member 11 [Homo sapiens]
 gi|37182003|gb|AAQ88805.1| RGNL596 [Homo sapiens]
 Length = 271

Score = 812 bits (1907), Expect = 0.0

Identities = 262/271 (96%), Positives = 262/271 (96%), Gaps = 7/271 (2%)

Query: 1 MRGNLALVGVLLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60
 MRGNLALVGVLLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR
 Sbjct: 1 MRGNLALVGVLLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60

Query: 61 VGPTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR- 119
 VGPTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR
 Sbjct: 61 VGPTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRK 120

Query: 120 -IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP 178
 IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP
 Sbjct: 121 AIGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP 180

Query: 179 KDE-MNGL GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEE 233
 KDE NGL YLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN RSGEPNNAYDEE
 Sbjct: 181 KDEAANGLMAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEE 240

Query: 234 DCVEMVASGGWNDVACHTTMYFMCEFDKENM 264
 DCVEMVASGGWNDVACHTTMYFMCEFDKENM
 Sbjct: 241 DCVEMVASGGWNDVACHTTMYFMCEFDKENM 271

>gi|38049424|ref|XP_283054.2| collectin sub-family member 11 [Mus musculus]
 gi|12832584|dbj|BAB22581.1| unnamed protein product [Mus musculus]
 Length = 272

Score = 736 bits (1728), Expect = 0.0

Identities = 242/271 (89%), Positives = 253/271 (93%), Gaps = 8/271 (2%)

Query: 1 MRGNLALVGVLLISLAFLSLLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60
 MR +LAL G+LISLAFLSLLPSG PQ +DACSVQILVPGLKGDAGEKGDKGAPGRPGR
 Sbjct: 3 MR-DIALAGMLISLAFLSLLPSGCPQQTEDACSVQILVPGLKGDAGEKGDKGAPGRPGR 61

Query: 61 VGPTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR- 119
 VGPTGEKGDMDGDKGQKG+VGRHGKIGPIG+KGEKGDSDIGPPGP+GEPG+PCECSQLR
 Sbjct: 62 VGPTGEKGDMDGDKGQKGTVGRHGKIGPIGAKGEKGDSDIGPPGPSGEPIPCCECSQLRK 121

Query: 120 -IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMP 178
 IGEMDNQV+QLT+ELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQ RGGTLSMP
 Sbjct: 122 AIGEMDNQVTQLTTELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQARGGTLSMP 181

Query: 179 KDE-MNGL--GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEE 233
 KDE NGL YLAQAGLARVFIGINDLEKEGAFVYSD SPM+TFN RSGEPNNAYDEE

Sbjct: 182 KDEAANGLMASYLAQAAGLARVFIGINDLEKEGAFVYSDRSPMQTFNKWRSGE PNNAYDEE 241

Query: 234 DCVEMVASGGWNDVACHTTMYFMCEFDKENM 264
DCVEMVASGGWNDVACH TMYFMCEFDKEN+

Sbjct: 242 DCVEMVASGGWNDVACHTTMYFMCEFDKENL 272

>gi|34863397|ref|XP_345653.1| similar to hypothetical protein MGC3279 similar
[Rattus norvegicus]
Length = 319

Score = 719 bits (1689), Expect = 0.0

Identities = 239/282 (84%), Positives = 254/282 (90%), Gaps = 19/282 (6%)

Query: 1 MRGNLALVGVLLISLAFLSLLPSGHPQAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGR 60
MR +LAL G+LISLAELSLLPSG PQ +DACSVQILVPGLKGD+GEKG+KGAPGRPGR

Sbjct: 39 MR-DLALAGMLISLAELSLLPSGCPQQTTFEDACSVQILVPGLKGDSEKGNKGAPGRPGR 97

Query: 61 VGPTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEP----- 109
VGPTGEKGDMDGDKGQKG+VGRHGKIGPIG+KGEKGDSDIGPPGP+GEP

Sbjct: 98 VGPTGEKGDMDGDKGQKGTVGRHGKIGPIGAKGEKGDSDIGPPGPSGEPASPMNRLHT 157

Query: 110 GLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLS 167
G+PCECSQLR IGEMDNQV+QLT+E+KFIKNAVAGVRETESKIYLLVKEEKRYADAQLS

Sbjct: 158 GIPCECSQLRKAIGEMDNQVQLTTEIKFIKNAVAGVRETESKIYLLVKEEKRYADAQLS 217

Query: 168 CQGRGGTSLMPKDE-MNGL--GYLAQAAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--R 222
CQGRGGTSLMPKDE NGL YLAQAAGLARVFIGINDLE+EGAFVYSD SPM+TFN R

Sbjct: 218 CQGRGGTSLMPKDEAANGLMASYLAQAAGLARVFIGINDLEREGAFVYSDRSPMQTFNKWR 277

Query: 223 SGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEFDKENM 264
SGEPNNAYDEEDCVEMVASGGWNDVACH TMYFMCEFDKEN+

Sbjct: 278 SGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEFDKENL 319

>gi|40548420|ref|NP_954705.1| collectin sub-family member 11 isoform b [Homo s
gi|31455215|gb|AAH09951.1| Collectin sub-family member 11, isoform b [Homo sapi
Length = 268

Score = 609 bits (1429), Expect = e-173

Identities = 195/204 (95%), Positives = 195/204 (95%), Gaps = 7/204 (3%)

Query: 68 GDMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR--IGEMDN 125
GDMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLR IGEMDN

Sbjct: 65 GDMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPGLPCECSQLRKAIGEMDN 124

Query: 126 QVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTSLMPKDE-MNG 184
QVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTSLMPKDE NG

Sbjct: 125 QVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTSLMPKDEAANG 184

Query: 185 L--GYLAQAAGLARVEIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEEDCVEMVA 240
L YLAQAAGLARVFIGINDLEKEGAFVYSDHSPMRTFN RSGEPNNAYDEEDCVEMVA

Sbjct: 185 LMAAYLAQAAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVA 244

Query: 241 SGGWNDVACHTTMYFMCEFDKENM 264
SGGWNDVACHTTMYFMCEFDKENM

Sbjct: 245 SGGWNDVACHTTMYFMCEFDKENM 268

>gi|33417124|gb|AAH56052.1| Colec11-prov protein [Xenopus laevis]
Length = 271

Score = 569 bits (1336), Expect = e-161
Identities = 201/262 (76%), Positives = 223/262 (85%), Gaps = 7/262 (2%)

Query: 9 GVLISLAFSLSLPSGHPQPAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVGPTEGKG 68
G +ISL FL LL SG+ Q D+ CSVQILVPGLKGDAGEKG+KGAPGRPGRVGP GEKG
Sbjct: 9 GVLISLGFLLILLGSGYQCQHITDETCSVQILVPGLKGDAGEKGEKGAPGRPGRVGPPEGKG 68

Query: 69 DMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEPLPCECSQLR--IGEMDNQ 126
++GDKG KGS+GRHGKIGPIGSKGEKGD G IGPPGPNGEPLPCEC QLR +GEMD Q
Sbjct: 69 EIGDKGIKGSMDRGHGKIGPIGSKGEKGDVGQIGPPGPNGEPLPCECQQLRKAVGEMDIQ 128

Query: 127 VSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTSLMPKDE-MNGL 185
V+QL +E+KF+KN VAGVRETE+KIYLLVKEEK+Y DAQ CQGRGGTSLMPKDE N L
Sbjct: 129 VAQLATEVKFVKNVVAGVRETETKIYLLVKEEKYIDAQDYCQGRGGTSLMPKDEATNSL 188

Query: 186 --GYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFN--RSGEPNNAYDEEDCVEMVAS 241
Y+ AGL+RVFIGINDLE+EG FVYSD SPM+TFN R EPNNAYDEEDC EMV+S
Sbjct: 189 IASYINHAGLSRVFIGINDLEREGHIFVYSDRSPMQTFNKWRQAEPNNAYDEEDCAEMVSS 248

Query: 242 GGWNDVACHTTMYFMCEFDKEN 263
GGWNDV+C TMYF+CEFDKEN
Sbjct: 249 GGWNDVSCHTTMYFICEFDKEN 270

>gi|277189011|ref|XP_235330.1| similar to collectin liver 1; collectin-L1 [Ratt]
Length = 277

Score = 246 bits (574), Expect = 9e-64
Identities = 118/231 (51%), Positives = 167/231 (72%), Gaps = 15/231 (6%)

Query: 40 PGLKGDAGEKGDKGAPGRPGRVG---PTGEKGDMDGDKGQKGSVGRHGKIGPIGSKGEKGD 96
PG KGD GE+GD G G+ G+VG P G KG++GD G +G +G K GPIG KG+KG+
Sbjct: 46 PGPKGDNNGERGDTGEEGKDGKVGRQGPVKVKGELGDMCAQGDIG--KSGPIGKKGDKGE 102

Query: 97 SGDIGPPGPNGEPLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLL 154
G +G PG G+ G C+C + R +G++D V++L + +KFIKN +AG+RETE K Y +
Sbjct: 103 KGLLGVPGEKGKAGTICDCGRYRKVVQQLDISVARLKTSMKFIKNVIAGIRETEEFYFI 162

Query: 155 VKEEKRYADAQLS-CQGRGGTSLMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFV 210
V+EEK Y ++ L+ C+ RGG L+MPKDE+ N L Y+A++G RVFIG+NDLEKEG +V
Sbjct: 163 VQKEKNYRES-LTHCRIRGGMAMPKDEVVNPLIADYVAKSGFFRVFIGVNDLEKEGQYV 221

Query: 211 YSDIISPMRTFN--RSGEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259
++D++P++ ++ + GEP++ Y EDCVEM++SG WND CH TMYF+CEF
Sbjct: 222 FTDNTPLQNYSNWKEGEPSPDPYGHEDCVEMLSSGRWNDTECHLTMYFVCEF 272

>gi|5453619|ref|NF_006429.1| collectin sub-family member 10; collectin liver 1
[Homo sapiens]

gi|5162875|dbj|BAAB1747.1| collectin 34 [Homo sapiens]
Length = 277

Score = 244 bits (569), Expect = 4e-63

Identities = 116/231 (50%), Positives = 167/231 (72%), Gaps = 15/231 (6%)

Query: 40 PGLKGDAGEKGDKGAPGRPRGRVG---PTGEKGMGDKGQKGSVGRHKGKIGPIGSKGEKGD 96
 PG KGD GEKGD G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+

Sbjct: 46 PGPKGDDGEKGDPEEGKHGKVGVRMGPKGIKGEKGDMGDRGNIG---KTGP1GKKGDKGE 102

Query: 97 SGD1GPPPGNGEPGLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLL 154
 G +G PG G+ G C+C + R +G++D +++L + +KF+KN +AG+RETE K Y +



Sbjct: 103 KGLLGIPGEKKGAGTVCD CGRYRK FVGQLDISIARLKTSMKFVKNVIA GIRETEEFYI 162

Query: 155 VKEEKRYADAQLS-CQGRGGTSLMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFV 210
 V+EEK Y ++ L+ C+ RGG L+MPKDE N L Y+A++G RVFIG+NDLE+EG ++

Sbjct: 163 VQEEKNYRES-LTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYM 221

Query: 211 YSDHSPMRTE-NRS-GEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259
 ++D++P++ + N + GEP++ Y EDCVEM++SG WND CH TMYF+CEF

Sbjct: 222 FTDNTP1QNYSNWNEGEPSDPYGHEDCVEMLSSGRWNDTECHLTMYFVCEF 272

 >gi|37183194|gb|AA089397.1|  COLEC10 [Homo sapiens]
 Length = 277

Score = 239 bits (557), Expect = 1e-61

Identities = 116/231 (50%), Positives = 166/231 (71%), Gaps = 15/231 (6%)

Query: 40 PGLKGDAGEKGDKGAPGRPRGRVG---PTGEKGMGDKGQKGSVGRHKGKIGPIGSKGEKGD 96
 PG KGD GEKGD G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+

Sbjct: 46 PGPKGDDGEKGDPEEGKHGKVGVRMGPKGIKGEKGDMGDRGNIG---KTGP1GKKGDKGE 102

Query: 97 SGD1GPPPGNGEPGLPCECSQLR--IGEMDNQVSQLTSELKFIKNAVAGVRETESKIYLL 154
 G +G PG G+ G C+C + R +G++D +++L + +KF+KN +AG+RETE K Y +




Sbjct: 103 KGLLGIPGEKKGAGTVCD CGRYRK FVGQLDISIARLKTSMKFVKNVIA GIRETEEFYI 162

Query: 155 VKEEKRYADAQLS-CQGRGGTSLMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFV 210
 V+EEK Y ++ L+ C+ RGG L+MPKDE N L Y+A++G RVFIG+NDLE+EG ++

Sbjct: 163 VQEEKNYRES-LTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYM 221

Query: 211 YSDHSPMRTE-NRS-GEPNNAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259
 ++D++P++ + N + GEP++ Y EDCVEM++SG WND CH TMYF+CEF

Sbjct: 222 STDNTP1QNYSNWNEGEPSDPYGHEDCVEMLSSGRWNDTECHLTMYFVCEF 272

 >gi|277341381|ref|NF_775598.1|  collectin liver 1; collectin-L1 [Mus musculus]
 gi|26324374|gb|BAC25941.1|  unnamed protein product [Mus musculus]
 Length = 277

Score = 234 bits (546), Expect = 3e-60

Identities = 128/280 (45%), Positives = 185/280 (66%), Gaps = 36/280 (12%)

Query: 1 MRGNLA--LVGVLI SLAFLSLLP SGHPQPAG---D-----DACSVQIILVPGIKGDAGEKG 50
 +R NL+ LV L+LL H Q G D + C+ + PG KGD GE+G

Sbjct: 8 LRSNLSMLLV-----LALL---HFQSLGLD VDSRSAAEVCATHTISPGPKGDDGGRG 56

Query: 51 DKGAPGRPRGRVG---PTGEKGMGDKGQKGSVGRHKGKIGPIGSKGEKGD SGD1GPPPGNG 107
 D G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+ G +G PG G

Sbjct: 57 DTGEEGKDGKVGRQGPKGVKGELGDMGAQGNIG---KSGPIGKKGDKGEKGLLGIPGEKG 113

Query: 108 EPGLPCECSQLR--IGEMDNQVSQITSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQ 165
+ G C+C I R +G++D V++L + +KFIKN +AG+RETE K Y +V+EEK Y ++

Sbjct: 114 KAGTICDCGRYRKVVGGQLDISVARLKTSMKFIKNVIAGIRETEEEKFYIYVQEEKNYRES- 172

Query: 166 LS-CQGRGGTSLMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFVYS DHSPMRTFN 221
L+ C+ RGG L+MPKDE+ N L Y+A++G RVEFIG+NDLE+EG +V++D++P++ ++

Sbjct: 173 LTHCRIRGGMLAMPKDEVVNTLIADYVAKSGFFRVFIGVNDLEREGQYVFTDNTPLQNYNS 232

Query: 222 --RSGEPNNAAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259
+ EP++ EDCVEM++SG WND CH TMYF+CEF

Sbjct: 233 NWKEEPEPSIDPSGHEDCVEMLSSGRWNDTECHLTMYFVCEF 272

>gi|27530341|gb|BAC53954.1| collectin-L1 [Mus musculus]
Length = 277

Score = 233 bits (544), Expect = 6e-60
Identities = 127/278 (45%), Positives = 185/278 (66%), Gaps = 32/278 (11%)

Query: 1 MRGNLALVGVLI SLAFLSLLPSGHPQAG---D-----DACSQILVPLKGDAGEKGDK 52
+R NL++ L L+LL H Q G D + C+ + PG KGD GE+GD

Sbjct: 8 LRSNLSM-----L LLLALL---HFQSLGLD VDSRSAAEVCATHTISPGPKGDDGERGDT 58

Query: 53 GAPGRPGRVG---PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPNGEF 109
G G+ G+VG P G KG++GD G +G++G K GPIG KG+KG+ G +G PG G+

Sbjct: 59 GEEGKDGKVGRQGPKGVKGELGDMGAQGNIG---KSGPIGKKGDKGEKGLLGIPGEKGKA 115

Query: 110 GLPCECSQLR--IGEMDNQVSQITSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLS 167
G C+C + R +G++D V++L + +KFIKN +AG+RETE K Y +V+EEK Y ++ L+

Sbjct: 116 GTICDCGRYRKVVGGQLDISVARLKTSMKFIKNVIAGIRETEEEKFYIYVQEEKNYRES-LT 174

Query: 168 -CQGRGGTSLMPKDEM-NGL--GYLAQAGLARVFIGINDLEKEGAFVYS DHSPMRTFN-- 221
C+ RGG L+MPKDE+ N L Y+A++G RVEFIG+NDLE+EG +V++D++P++ ++

Sbjct: 175 HCRIRGGMLAMPKDEVVNTLIADYVAKSGFFRVFIGVNDLEREGQYVFTDNTPLQNYNSW 234

Query: 222 RSGEPNNAAYDEEDCVEMVASGGWNDVACHTTMYFMCEF 259
+ EP++ EDCVEM++SG WND CH TMYF+CEF

Sbjct: 235 KEEEPSIDPSGHEDCVEMLSSGRWNDTECHLTMYFVCEF 272

>gi|7656989|ref|NP_056534.1| collagen, type V, alpha 3 preproprotein; pro-(alp
[Homo sapiens])

gi|34223720|sp|P25940|CA35 HUMAN Collagen alpha 3(V) chain precursor
gi|7329074|gb|AAF59902.1| collagen type V alpha 3 chain [Homo sapiens]
Length = 1745

Score = 78.7 bits (178), Expect = 3e-13
Identities = 48/92 (52%), Positives = 53/92 (57%), Gaps = 24/92 (26%)

Query: 39 VPGLKGDAGEKGDGK---APGRPGRVGPTGEKGMGDKGQKGSVGR---HGKIGP----- 87
+PG KGD GEKGD G A G PG+ GP GE D G KGSVG G +GP

Sbjct: 1221 IPGPKGDIGEKGDSPSGAAGPPCKKGPPGE-----D-GAKGSVGP TGI PGDLGPPGDPG 1274

Query: 88 ---I-GSKGEKGDSDIGI--GPPGPNGEPLP 112
I GS GEKGD GD+ GPPG +GEPPG P

Sbjct: 1275 VSGIDGSPGEKGDGPGDVGGPGPPGASGEPGAP 1306

Score = 59.6 bits (133), Expect = 2e-07

Identities = 46/117 (39%), Positives = 50/117 (42%), Gaps = 51/117 (43%)

Query: 47 GEKGDKGAPG-----R--PGRVGP-----TGM----- 66
 GEKG KG PG R PGRVGP GM
 Sbjct: 1325 GEKGAKGEPGPDGPPGRITGPMGARGPPGRVGPGLRGIPGFPVGEPLLLGAPGQMGPPI'L 1384

Query: 67 -----KGDMDKGQKGSVGRHGKIGPIGSKGEKGD)SG--DI-GPPGPNGEPGLP 112
 KGD G KG+KG +G G IGP G GEKGD G + GPPGP G+PG P
 Sbjct: 1385 GPSGLPGLKGDTPKGEKGHIGLIGLIGPPGEAGEKGDQGLPGVQGPPGPKGDPGPP 1441

Score = 55.4 bits (123), Expect = 3e-06

Identities = 42/109 (38%), Positives = 46/109 (42%), Gaps = 48/109 (44%)

Query: 40 PGLKGD-----AGEKGD-----KGAPGRPGRV----- 61
 PGLKGD AGEKGD KG PG PG +
 Sbjct: 1390 PGLKGDTPKGEKGHIGLIGLIGPPGEAGEKGDQGLPGVQGPPGPKGDPGPPGPICSLGH 1449

Query: 62 -GPTGEKGDMDKGQKGSVGRHGKIGPIGSKGEKGD)SGDIGPPGPNGEP 109
 GP G G +G KG KGS P GS G +GD+G GPPGP G P
 Sbjct: 1450 PGPPGVAGPLGQKGSKCS-----P-GSMGPRGDTGPAGPPGPPGAP 1489

Score = 54.9 bits (122), Expect = 4e-06

Identities = 50/129 (38%), Positives = 59/129 (45%), Gaps = 50/129 (38%)

Query: 21 PSGHPPQAGDDACSVQILV-----PGL----KGDA)GEKGDK ---GAPGRPGRVGPPTGEK 67
 P+GHP P G D Q PGL KGD) G +G G PG G GP GEK
 Sbjct: 1107 PAGHPGPPGADG--AQ---GRRGPPGLFGQKGD)GVVRG--FVGVIGPPGLQGLPGPPGEK 1159

Query: 68 GDMGDKGQKGSVGRHGKIGP-----IGSKGEKGD)SGDIGPP 103
 G++GD G S+G HG GP +G KGE+GD+GD P
 Sbjct: 1160 GEVGDVG---SMGPHGAPGPRGPQGPTGSEGTPLPGGVGQPGAVGEKGERGDAGD---P 1213

Query: 104 GPNGEPGLP 112
 GP G PG+P
 Sbjct: 1214 GPPGAPGIP 1222

Score = 53.7 bits (119), Expect = 1e-05

Identities = 41/92 (44%), Positives = 46/92 (50%), Gaps = 28/92 (30%)

Query: 44 GDAGEKGDK-----GAPGRPGR-----VGPTGEKGDMDKGQKGSVG RHGKIG 86
 G AGEKG K G PGRPG +GP GEKG G GQ G G R G
 Sbjct: 779 GSAGEKG-KLGVPGLPGYPGRPGPKGSIGFPGPLGPIGEKGKSKKTGQPGLECER----G 833

Query: 87 PIGSKGEKGD)SGDIGPPGPNGE-----PGLP 112
 P GS+GE+G G G PGP G+ PG+P
 Sbjct: 834 PPGSRGERGQPGATGQPGPKGDVGDGAPGIP 865

Score = 53.2 bits (118), Expect = 1e-05
Identities = 35/79 (44%), Positives = 39/79 (49%), Gaps = 27/79 (34%)

Query: 40 PGLKGDAGEKGDKGAPGRPRVGPTEGEKGDMDGDKQKGSVGRHGKIGPIGSKGEKGDSDG 99
PG KGD G KGD+G PG PG P GE D GP G KG+ G +G+
Sbjct: 736 PGEKGDVGLKGDQKPGAPG---PRGE-----D-----GPEGPKGQAGQAGE 774

Query: 100 IGPPGPNGE-----PGLP 112
GPPG GE PGLP
Sbjct: 775 EGPPGSAGEKKGKLGVPGLP 793

Score = 50.3 bits (111), Expect = 1e-04
Identities = 43/104 (41%), Positives = 50/104 (48%), Gaps = 36/104 (34%)

Query: 40 PGLKGDAGEKGDKGA-----P-GRPGRVG-----P--TGEKGDMDG----- 71
PGLKG+ G +G +G P G PGRVG P TG KGD G
Sbjct: 499 PGLKGEEGAEGPQGPRGLQGPHPGRVGMGRPGADGARGLPGDTGPKGDRGFDGLPGL 558

Query: 72 --DKGQKGSVGRHGKIGPIGSKGEKGDSDIGPPGPN---GEPG 110
+KGQ+G G G+ GP GE G+ G GPPGP GEPG
Sbjct: 559 PGEKQQRGDFGHVGPQP---PGEDGERGAEGPPGPTGQAGEPG 599

Score = 49.4 bits (109), Expect = 2e-04
Identities = 39/94 (41%), Positives = 50/94 (53%), Gaps = 26/94 (27%)

Query: 40 PGLKGDAGE-----KGDKGAPGRPRVGPTEG-----EKGDMDGDKQKGSVGRHG 83
PG KGD G+ G+ GAPG PG+ GP+G E G+ G KG+ G G G
Sbjct: 1282 PGEKGDVGDVGGPGPPGASGEPGAPGPPGKRGPSCMHMGREGRE-GEKGAKGEPGPDGPPG 1340

Query: 84 KIGPIGSKGEMKGDSDIGP-----PGPNGEPL 111
+ GP+G+G G +GP PGP GEPGL
Sbjct: 1341 RTGPMGARGP ---PGRVGPEGLRGIPGPVGPGL 1371

Score = 47.7 bits (105), Expect = 7e-04
Identities = 31/63 (49%), Positives = 33/63 (52%), Gaps = 18/63 (28%)

Query: 56 GRPGRVGPTEGEKGDMDGDKQKGSVGRHGKIGPIGSKGEKGDSDIGPP-----GPNGEP 109
G PG GP+GE+GD GD VG P G KG KGD GD GPP GP G P
Sbjct: 1064 GPPGAAGPSGEEGDKGD-----VG-----AP-GHKGSKGDKGDAGPPGQPGIRGPAGHP 1111

Query: 110 GLP 112
G P
Sbjct: 1112 GPP 1114

Score = 46.0 bits (101), Expect = 0.002
Identities = 44/127 (34%), Positives = 54/127 (42%), Gaps = 58/127 (45%)

Query: 40 PGLKGDAGE-----KGDKGAPG-----R-----PGR-----VGPTGE 66
PG KG G+ KGDKG PG R PG+ VGP G+
Sbjct: 979 PGPKGGPGDPGPTGLKGDKGPPGPGVANGSPGERGPLGPAGGIGLPGQSGSEGPVGPAGK 1038

Query: 67 KGDMDGDKQKGSVGRHGKI-GPIG-----SKGEKGDSDIGPP----- 103